

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:17:16 ; Search time 52.57 Seconds
(without alignments)
147.151 Million cell updates/sec

Title: US-09-331-631A-24_COPY_29_94

Perfect score: 382
Sequence: 1 HDEDDRRGSHSLQCCVORC.....EQEEDGRCRGWHEGGEREE 66

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 segs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_15:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mhvc:*
8: sp_mammal:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	382	100.0	637	10 003678	003678 hordeum vul
2	138	36.1	582	10 003865	003865 zea mays (m
3	136	35.6	238	10 081257	081257 zea luxuria
4	135	35.3	238	10 081249	081249 zea mays su
5	135	35.3	238	10 081255	081255 zea mays su
6	135	35.3	238	10 09SBE8	09SBE8 zea mays su
7	135	35.3	240	10 09SBEF0	09SBEF0 zea mays su
8	135	35.3	240	10 09SBE9	09SBE9 zea mays su
9	135	35.3	242	10 081251	081251 zea mays su
10	135	35.3	242	10 09SBE6	09SBE6 zea mays su
11	135	35.3	407	10 041750	041750 zea mays (m
12	134	35.1	238	10 09SBE5	09SBE5 zea luxuria
13	134	35.1	238	10 09SBE6	09SBE6 zea luxuria
14	133	34.8	238	10 081258	081258 zea luxuria
15	133	34.8	240	10 081252	081252 zea mays su
16	133	34.8	240	10 081256	081256 zea mays su
17	133	34.8	240	10 09SBE7	09SBE7 zea mays su
18	133	34.8	540	10 003866	003866 zea mays (m
19	132	34.6	239	10 09SBEF1	09SBEF1 zea mays su

20	130	34.0	239	10 081253	081253 zea mays su
21	129.5	33.9	122	10 003863	003863 zea mays (m
22	127	33.2	236	10 081254	081254 zea mays su
23	125.5	32.9	246	10 081261	081261 tripacum d
24	125	32.7	236	10 09SBE2	09SBE2 zea mays su
25	124.5	32.6	242	10 081260	081260 tripacum d
26	116	30.4	236	10 081250	081250 zea mays su
27	115	30.1	666	10 09SPL5	09SPL5 macadamia i
28	111.5	29.2	242	10 081259	081259 tripacum d
29	105	27.5	666	10 09SPL4	09SPL4 macadamia i
30	97	25.4	393	10 09ZRP0	09ZRP0 oryza sativ
31	92	24.1	625	11 099053	099053 ratius norv
32	91	23.8	402	10 09ZRH8	09ZRH8 oryza sativ
33	91	23.3	625	10 09SPL3	09SPL3 macadamia i
34	85	22.3	593	10 09SEW4	09SEW4 juglans reg
35	76.5	20.0	566	10 024294	024294 pisum sativ
36	75	19.6	512	5 09VRD5	09VRD5 drosophila
37	75	19.6	699	4 094769	094769 homo sapien
38	74.5	19.5	1655	5 024754	024754 drosophila
39	73.5	19.2	239	12 09QME3	09QME3 avian endog
40	73.5	19.2	261	13 093368	093368 xenopus lae
41	73.5	19.2	810	10 09ZM13	09ZM13 cucurbita m
42	73	19.1	532	2 052993	052993 escherichia
43	72	18.8	525	10 043358	043358 theobroma c
44	72	18.8	818	5 09VJ77	09VJ77 drosophila
45	71	18.6	57	4 09Y4J1	09Y4J1 homo sapien

ALIGNMENTS

RESULT 1
ID 003678 PRELIMINARY: PRT: 637 AA.

AC 003678; 01-NOV-1996 (TREMUREL. 01, Created)
DT 01-NOV-1996 (TREMUREL. 01, Last sequence update)
DT 01-OCT-2000 (TREMUREL. 15, Last annotation update)
DE FERTIL STORAGE PROTEIN.
GN BEG1 OR GBL1.
OS Hordeum vulgare (Barley), and Triticum aestivum (wheat).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.
OX NCBI_Taxid=4513; 4565;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93287986; PubMed=8510647;
RA Heck G.R., Chamberlain A.C., Ho T.H.D.;
RT "Barley embryo globulin 1 gene, Beg1: characterization of cDNA,
RT chromosome mapping and regulation of expression.";
RL Mol. Gen. Genet. 239:209-218(1993).
DR EMBL: M64372; AAA32936.1; -;
DR EMBL: M61719; AAA34269.1; -;
DR HSSP: P02853; 2PHL.
DR MENDEL: 8553; Horvu:1188; 8553.
DR INTERPRO: IPR000901; -;
DR INTERPRO: IPR001113; -;
PRAM: PF00546; SeedStore_7s; 1.
DR PROSITE: PS00867; CPASASE_2; UNKNOWN_1.
DR PRODOM: PD081059; -; 1.
KW Seed storage protein.
SQ SEQUENCE 637 AA; 72252 MW; F323F4FF9947C3C CRC64;

Query Match 100.0%; Score 382; DB 10; Length 637;
Best Local Similarity 100.0%; Pred. No. 7.4e-37;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDEDDRRGSHSLQCCVORCROEPRYSHARCVOECDDDOOHGRHQEEEGRGRRMG 60
Db 29 HDEDDRRGSHSLQCCVORCROEPRYSHARCVOECDDDOOHGRHQEEEGRGRRMG 88
QY 61 EGEREE 66

Db 89 EGEREE 94

RESULT 2

ID 003865 PRELIMINARY; PRT; 582 AA.

AC 003865;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, last annotation update)
DE VITCIN-LIKE EMBRYO STORAGE PROTEIN.

GN GIB1-L.
OS Zea mays (maize).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
OX NCBI_TaxId=4577;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN-W64A;
RX MEDLINE-92090707; PubMed-1752424;
RA Belanger F.C., Kriz A.L.;

RT "Molecular basis for allelic polymorphism of the maize globulin-1

gene.";
RL Genetics 129:863-872(1991).
DR EMBL; X59083; CAA1809.1; -.
DR HSSP; P50477; ICAU.

DR MENDEL; 11234; Zeama; 1188; 11234.

DR INTERPRO; IPR000901; -.
DR INTERPRO; IPR001113; -.

DR PRAM; PR00546; Seedstore_7s; 1.
DR PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
DR PRODOM; PD081059; -; 1.
KW Seed storage protein.

SQ SEQUENCE 582 AA; 66162 MW; 680D85FEC07CB885 CRC64;

Query Match 36.1%; Score 138; DB 10; Length 582;
Best Local Similarity 37.7%; Pred. No. 2e-08;

Matches 26; Conservative 14; Mismatches 21; Indels 8; Gaps 3;

OY 2 DDEDDRRGSHLQOCVORCROERPRYSHARCVOECRDDQ---QOHGRHDEEEGCGRG 57

Db 26 DDNNHHHGKSGRCVYARC-EDRPWHORPCLQCREREKROERSRHADDSGSG-- 82

OY 58 WHGEGEREE 66

Db 83 -SSEDEREQ 90

RESULT 3

ID 081257 PRELIMINARY; PRT; 238 AA.

AC 081257;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, last annotation update)
DE GLOBULIN-1 (FRAGMENT).

OS Zea luxurians (Teosinte).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
OX NCBI_TaxId=15945;
RN 11
RP SEQUENCE FROM N.A.
RA Hilton H., Gaut B.S.;

RT "Speciation and domestication in maize and its wild relatives:
evidence from the globulin-1 gene.";
RL Genetics 0:0-0(1998).
DR EMBL; AF064228; AAC31471.1; -.
DR HSSP; P50477; ICAU.

DR MENDEL; 31899; Zealu; 1188; 31899.
DR INTERPRO; IPR000901; -.
DR INTERPRO; IPR001113; -.

DR PRAM; PR00546; Seedstore_7s; 1.
DR PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
DR NON_TER 238
SQ SEQUENCE 238 AA; 27233 MW; FD31A8066738E68 CRC64;

Query Match 35.6%; Score 136; DB 10; Length 238;

Best Local Similarity 36.2%; Pred. No. 1.6e-08;

Matches 25; Conservative 16; Mismatches 20; Indels 8; Gaps 3;

OY 2 DDEDDRRGSHLQOCVORCROERPRYSHARCVOECRDDQ---QOHGRHDEEEGCGRG 57

Db 26 DDNNHHHGKSGRCVYARC-EDRPWHORPCLQCREREKROERSRHADDSGSG-- 82

OY 58 WHGEGEREE 66

Db 83 -SSEDEREQ 90

RESULT 4

ID 081249 PRELIMINARY; PRT; 238 AA.

AC 081249;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, last annotation update)
DE GLOBULIN-1 (FRAGMENT).

OS Zea mays subsp. mays (maize).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
OX NCBI_TaxId=4578;
RN 11
RP SEQUENCE FROM N.A.
RA Hilton H., Gaut B.S.;

RT "Speciation and domestication in maize and its wild relatives:
evidence from the globulin-1 gene.";

RL Genetics 0:0-0(1998).
DR EMBL; AF064212; AAC31455.1; -.
DR HSSP; P50477; ICAU.

DR MENDEL; 31891; Zeama; 1188; 31891.

DR INTERPRO; IPR000901; -.
DR INTERPRO; IPR001113; -.

DR PRAM; PR00546; Seedstore_7s; 1.
DR PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
DR NON_TER 238

SQ SEQUENCE 238 AA; 27298 MW; EDF6A1DE3F86D0F0 CRC64;

Query Match 35.3%; Score 135; DB 10; Length 238;

Best Local Similarity 36.2%; Pred. No. 2e-08;

Matches 25; Conservative 16; Mismatches 22; Indels 6; Gaps 3;

OY 2 DDEDDRRGSHLQOCVORCROERPRYSHARCVOECRDDQ---QOHGRHDEEEGCGRG 57

Db 26 DDNNHHHGKSGRCVYARC-EDRPWHORPCLQCREREKROERSRHADDSGSGSS 84

OY 58 WHGEGEREE 66

Db 85 -EDEDEREQ 92

RESULT 5

ID 081255 PRELIMINARY; PRT; 238 AA.

AC 081255;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, last annotation update)
DE GLOBULIN-1 (FRAGMENT).

OS Zea mays subsp. parviglumis.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
OX NCBI_TaxId=76912;

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RN [1]
RP SEQUENCE FROM N.A.
RA Hilton H., Gaut B.S.;
RT "Speciation and domestication in maize and its wild relatives:
RT evidence from the Globulin-1 gene.";
RL Genetics 0:0-0(1998).
DR EMBL: AF064224; AAC31467.1; -.
DR MENDEL: 31897; Zeama;1188;31897.
DR INTERPRO: IPR000901; -.
DR INTERPRO: IPR001113; -.
DR PFAM: PF00546; Seedstore_7s; 1.
DR PROSITE: PS00867; CPSASE_2; UNKNOWN_1.
FT NON_TER 238
SQ SEQUENCE 238 AA; 27205 MW; 1186A5D6EB507E CRC64;

Query Match
Best Local Similarity 35.3%; Score 135; DB 10; Length 238;
Matches 26; Conservative 13; Mismatches 21; Indels 8; Gaps 3;

QY 2 DDEDDRGRGSHLQOCVORCROERPRYSARCVQECRDDQ---OQHGHEDEEGRG 57
DB 26 DDNHHNGHSGRCVRC-EDRPWQHPRCLQECREERERKQERSHHEADRSGGSS 82
QY 58 WHGEGERE 65
DB 83 -SSEDERE 89

RESULT 6
Q9SBE8 PRELIMINARY; PRT; 238 AA.
AC Q9SBE8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE GLOBULIN-1 (FRAGMENT).
OS Zea mays subsp. parviglumis.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
OX NCBI_TaxID=76912;
RN [1]
RP SEQUENCE FROM N.A.
RA Hilton H., Gaut B.S.;
RT "Speciation and domestication in maize and its wild relatives:
RT evidence from the Globulin-1 gene.";
RL Genetics 0:0-0(1998).
DR EMBL: AF064221; AAC31464.1; -.
DR HSSP: P50477; ICAU.
DR INTERPRO: IPR000901; -.
DR INTERPRO: IPR001113; -.
DR PFAM: PF00546; Seedstore_7s; 1.
DR PROSITE: PS00867; CPSASE_2; UNKNOWN_1.
FT NON_TER 238
SQ SEQUENCE 238 AA; 27362 MW; A75C0C7DED9B773A CRC64;

Query Match
Best Local Similarity 35.3%; Score 135; DB 10; Length 238;
Matches 25; Conservative 16; Mismatches 22; Indels 6; Gaps 3;

QY 2 DDEDDRGRGSHLQOCVORCROERPRYSARCVQECRDDQ---OQHGHEDEEGRG 57
DB 26 DDNHHNGHSGRCVRC-EDRPWQHPRCLQECREERERKQERSHHEADRSGGSS 84
QY 58 WHGEGERE 66
DB 85 -EDEREREQ 92

RESULT 7
Q9SBE0 PRELIMINARY; PRT; 240 AA.
AC Q9SBE0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE GLOBULIN-1 (FRAGMENT).
OS Zea mays subsp. parviglumis.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
OX NCBI_TaxID=76912;
RN [1]
RP SEQUENCE FROM N.A.
RA Hilton H., Gaut B.S.;
RT "Speciation and domestication in maize and its wild relatives:
RT evidence from the Globulin-1 gene.";
RL Genetics 0:0-0(1998).
DR EMBL: AF064220; AAC31463.1; -.
DR HSSP: P50477; ICAU.
DR INTERPRO: IPR000901; -.
DR INTERPRO: IPR001113; -.
DR PFAM: PF00546; Seedstore_7s; 1.
DR PROSITE: PS00867; CPSASE_2; UNKNOWN_1.
FT NON_TER 240
SQ SEQUENCE 240 AA; 27492 MW; ECD813393DC94AAC CRC64;

Query Match
Best Local Similarity 35.3%; Score 135; DB 10; Length 240;
Matches 25; Conservative 16; Mismatches 22; Indels 6; Gaps 3;

QY 2 DDEDDRGRGSHLQOCVORCROERPRYSARCVQECRDDQ---OQHGHEDEEGRG 57
DB 26 DDNHHNGHSGRCVRC-EDRPWQHPRCLQECREERERKQERSHHEADRSGGSS 84
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AC Q9SBE0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE GLOBULIN-1 (FRAGMENT).
OS Zea mays subsp. parviglumis.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
OX NCBI_TaxID=76912;
RN [1]
RP SEQUENCE FROM N.A.
RA Hilton H., Gaut B.S.;
RT "Speciation and domestication in maize and its wild relatives:
RT evidence from the Globulin-1 gene.";
RL Genetics 0:0-0(1998).
DR EMBL: AF064219; AAC31462.1; -.
DR HSSP: P50477; ICAU.
DR INTERPRO: IPR000901; -.
DR INTERPRO: IPR001113; -.
DR PFAM: PF00546; Seedstore_7s; 1.
DR PROSITE: PS00867; CPSASE_2; UNKNOWN_1.
FT NON_TER 240
SQ SEQUENCE 240 AA; 27499 MW; ECD813393DC94AAC CRC64;

Query Match
Best Local Similarity 35.3%; Score 135; DB 10; Length 240;
Matches 25; Conservative 16; Mismatches 22; Indels 6; Gaps 3;

QY 2 DDEDDRGRGSHLQOCVORCROERPRYSARCVQECRDDQ---OQHGHEDEEGRG 57
DB 26 DDNHHNGHSGRCVRC-EDRPWQHPRCLQECREERERKQERSHHEADRSGGSS 84
QY 58 WHGEGERE 66
DB 85 -EDEREREQ 92

RESULT 8
Q9SBE9 PRELIMINARY; PRT; 240 AA.
AC Q9SBE9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE GLOBULIN-1 (FRAGMENT).
OS Zea mays subsp. parviglumis.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
OX NCBI_TaxID=76912;
RN [1]
RP SEQUENCE FROM N.A.
RA Hilton H., Gaut B.S.;
RT "Speciation and domestication in maize and its wild relatives:
RT evidence from the Globulin-1 gene.";
RL Genetics 0:0-0(1998).
DR EMBL: AF064220; AAC31463.1; -.
DR HSSP: P50477; ICAU.
DR INTERPRO: IPR000901; -.
DR INTERPRO: IPR001113; -.
DR PFAM: PF00546; Seedstore_7s; 1.
DR PROSITE: PS00867; CPSASE_2; UNKNOWN_1.
FT NON_TER 240
SQ SEQUENCE 240 AA; 27492 MW; ECD813393DC94AAC CRC64;

Query Match
Best Local Similarity 35.3%; Score 135; DB 10; Length 240;
Matches 25; Conservative 16; Mismatches 22; Indels 6; Gaps 3;

QY 2 DDEDDRGRGSHLQOCVORCROERPRYSARCVQECRDDQ---OQHGHEDEEGRG 57
DB 26 DDNHHNGHSGRCVRC-EDRPWQHPRCLQECREERERKQERSHHEADRSGGSS 84
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Search completed: March 1, 2001, 16:17:16
job time: 454 sec
